A.

Exons: 1f   1e 1a 1d   1b   1c 2   3   4 5 6 7 8   9

Cosmids: J5 ──────────────

AE ──────────────

D2 ───

WE ──→

B.

ATG

1a   1c 2   3   45 6 7 8 9   [1]

1b   2

                                                            3

                                                            4

stop   5

┌ATG   ┌ATG

1d   [6]

                                                            7

                                                            8

                                                            9

stop   10

                      ┌ATG

1f   [11]

1e   12

                                                            13

                                                            14

C.

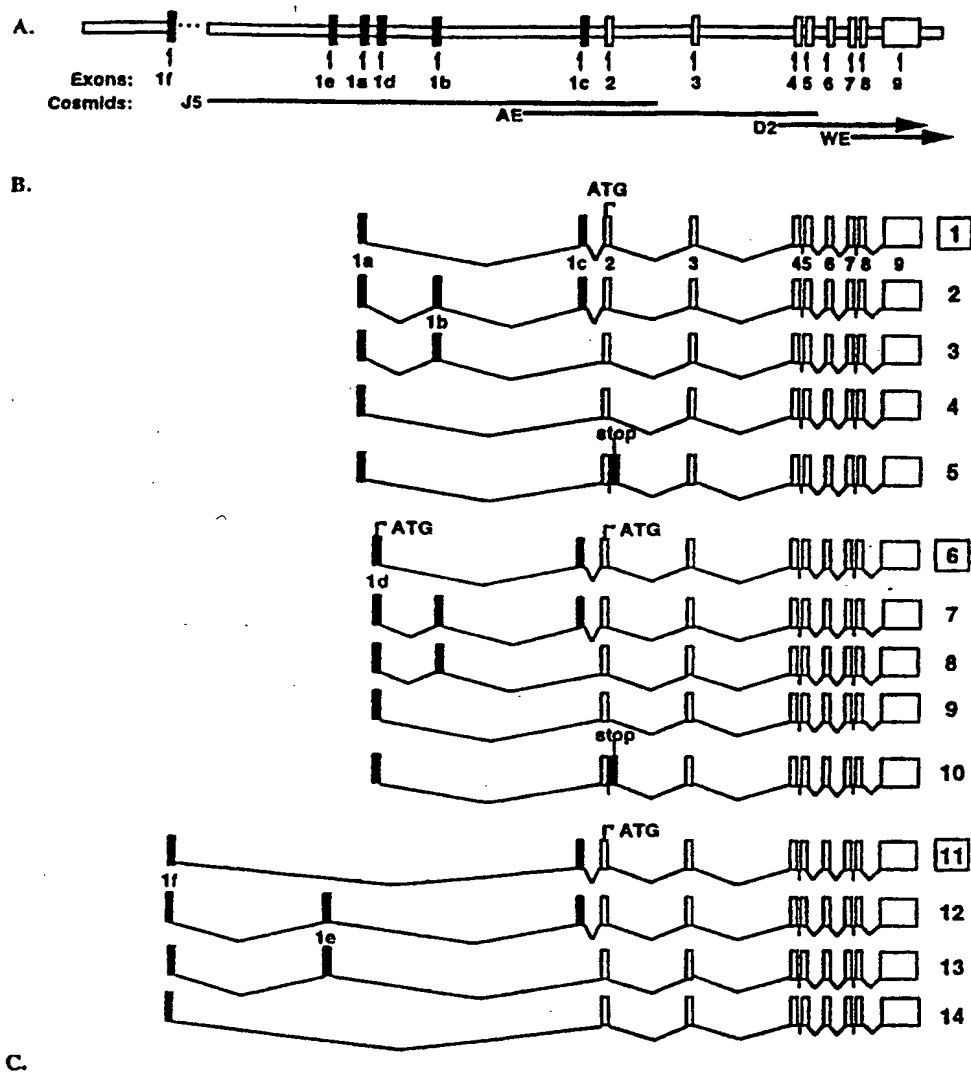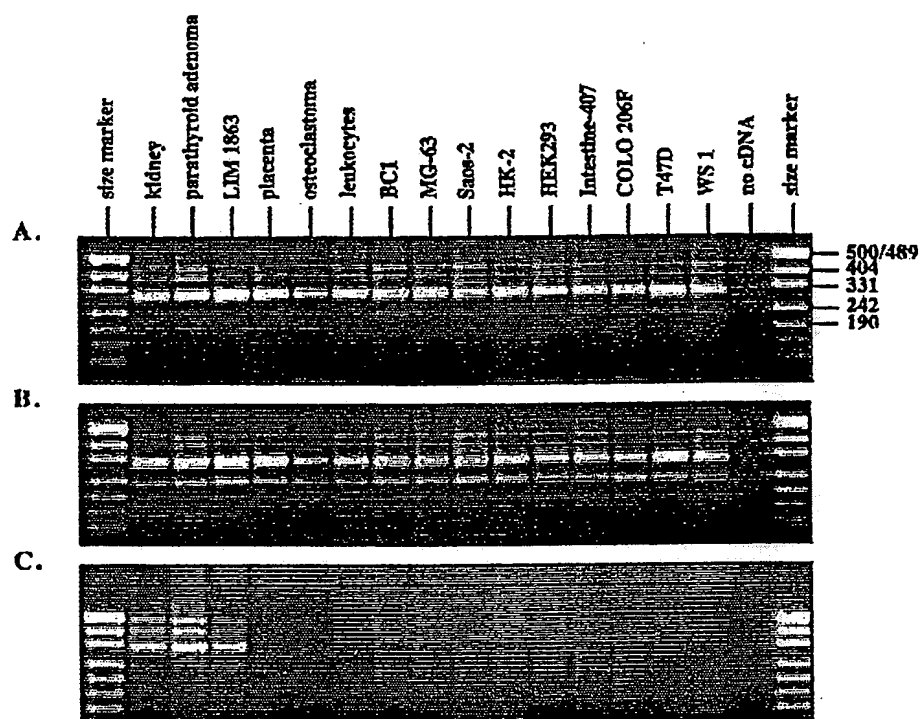Transcript 1:   MEAMA ASTSL PDPGD FDRNV PRI │ DBD │ 427aa

Transcript 6:   MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI │ DBD │ 477aa

Transcript 9:   MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNV PRI │ DBD │ 450aa

FIGURE 1

FIGURE 2
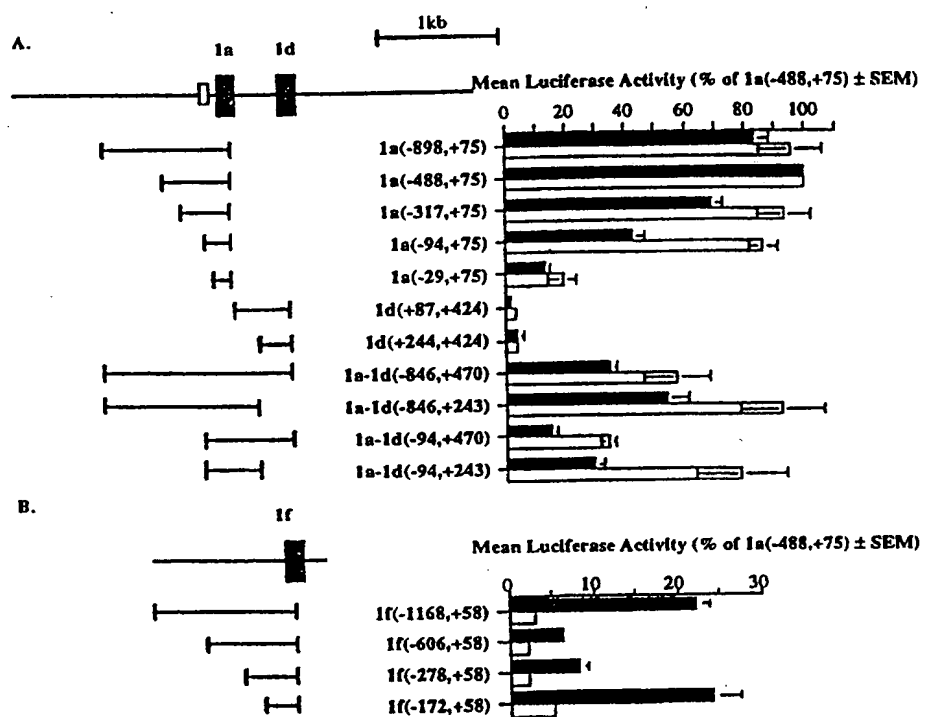
FIGURE 3

A.   5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3'

B.   5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3'

C.   5'...tgttttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3'

D.   5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGCATGGAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCGATGGTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3'

FIGURE 4

FIGURE 5   TRANSCRIPT 6

(Sequence Range: 1 to 1463)

```
            10         20         30         40         50
       *     *    *     *    *     *    *     *    *     *
     GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
     CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                        MetGluTrpArg AsnLysLys>


            60         70         80         90        100
       *     *    *     *    *     *    *     *    *     *
     AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
     TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
     ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>


           110        120        130        140        150
       *     *    *     *    *     *    *     *    *     *
     CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
     GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
      PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>


           160        170        180        190        200
       *     *    *     *    *     *    *     *    *     *
     CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
     GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
     SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>


           210        220        230        240        250
       *     *    *     *    *     *    *     *    *     *
     ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
     TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
     ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>


           260        270        280        290        300
       *     *    *     *    *     *    *     *    *     *
     TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
     ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
     GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>


           310        320        330        340        350
       *     *    *     *    *     *    *     *    *     *
     GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
     CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
     CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>


           360        370        380        390        400
       *     *    *     *    *     *    *     *    *     *
     TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
     AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
     PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

```
          410        420        430        440        450
           *    *     *    *     *    *     *    *     *    *
        CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
        GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
        HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

          460        470        480        490        500
           *    *     *    *     *    *     *    *     *    *
        AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
        TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
        LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

          510        520        530        540        550
           *    *     *    *     *    *     *    *     *    *
        CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
        GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
        LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

          560        570        580        590        600
           *    *     *    *     *    *     *    *     *    *
        GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
        CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
        SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

          610        620        630        640        650
           *    *     *    *     *    *     *    *     *    *
        AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
        TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
        LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

          660        670        680        690        700
           *    *     *    *     *    *     *    *     *    *
        CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
        GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
        ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

          710        720        730        740        750
           *    *     *    *     *    *     *    *     *    *
        CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
        GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
        ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

          760        770        780        790        800
           *    *     *    *     *    *     *    *     *    *
        TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
        AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
        IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

          810        820        830        840        850
           *    *     *    *     *    *     *    *     *    *
        AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
        TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
        SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```

7/20

```
          860        870        880       . 890        900
       *    *      *    *      *    *      *    *      *    *
    CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
    GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
    SerMetLeu  ProHisLeu  AlaAspLeuVal SerTyrSer IleGlnLys>


          910        920        930        940        950
       *    *      *    *      *    *      *    *      *    *
    TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
    AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
    ValIleGlyPhe AlaLysMet IleProGly  PheArgAspLeu ThrSerGlu>


          960        970        980        990        1000
       *    *      *    *      *    *      *    *      *    *
    GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
    CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
    AspGlnIle ValLeuLeuLys SerSerAla IleGluVal  IleMetLeuArg>


          1010       1020       1030       1040        1050
       *    *      *    *      *    *      *    *      *    *
    CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
    GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
    SerAsnGlu  SerPheThr  MetAspAspMet SerTrpThr CysGlyAsn>


          1060       1070       1080       1090        1100
       *    *      *    *      *    *      *    *      *    *
    AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
    TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
    GlnAspTyrLys TyrArgVal SerAspVal  ThrLysAlaGly HisSerLeu>


          1110       1120       1130       1140        1150
       *    *      *    *      *    *      *    *      *    *
    GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
    CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
    GluLeuIle  GluProLeuIle LysPheGln ValGlyLeu  LysLysLeuAsn>


          1160       1170       1180       1190        1200
       *    *      *    *      *    *      *    *      *    *
    CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
    GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
    LeuHisGlu  GluGluHis  ValLeuLeuMet AlaIleCys IleValSer>


          1210       1220       1230       1240        1250
       *    *      *    *      *    *      *    *      *    *
    CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
    GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
    ProAspArgPro GlyValGln AspAlaAla  LeuIleGluAla IleGlnAsp>


          1260       1270       1280       1290        1300
       *    *      *    *      *    *      *    *      *    *
    CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
    GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
    ArgLeuSer  AsnThrLeuGln ThrTyrIle ArgCysArg  HisProProPro>
```

```
                                                                       1350
                                              1340                    *    *
                                      1330    *    *
                1320           *      *
        1310    *      *                                    
*        *                                                                
GGGCAGCCAC  CTGCTCTATG  CCAAGATGAT  CCAGAAGCTA  GCCGACCTGC
CCCGTCGGTG  GACGAGATAC  GGTTCTACTA  GGTCTTCGAT  CGGCTGGACG
GlySerHis   LeuLeuTyr   AlaLysMetIle  GlnLysLeu  AlaAspLeu>


                                            1390           1400
                              1380          *    *         *    *
                   1370       *    *
          1360     *    *
*        *
GCAGCCTCAA  TGAGGAGCAC  TCCAAGCAGT  ACCGCTGCCT  CTCCTTCCAG
CGTCGGAGTT  ACTCCTCGTG  AGGTTCGTCA  TGGCGACGGA  GAGGAAGGTC
ArgSerLeuAsn  GluGluHis  SerLysGln  TyrArgCysLeu  SerPheGln>


                                          1440          1450
                              1430        *    *        *    *
                   1420       *    *
          1410     *    *
*        *
CCTGAGTGCA  GCATGAAGCT  AACGCCCCTT  GTGCTCGAAG  TGTTTGGCAA
GGACTCACGT  CGTACTTCGA  TTGCGGGGAA  CACGAGCTTC  ACAAACCGTT
ProGluCys   SerMetLysLeu  ThrProLeu  ValLeuGlu  ValPheGlyAsn>


          1460
          *      *
TGAGATCTCC  TGA
ACTCTAGAGG  ACT
GluIleSer   ***>
```

FIGURE 6   TRANSCRIPT 9

(Sequence Range: 1 to 1382)

```
          10        20        30        40        50
          *    *    *    *    *    *    *    *    *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                 MetGluTrpArg AsnLysLys>

          60        70        80        90        100
          *    *    *    *    *    *    *    *    *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

          110       120       130       140       150
          *    *    *    *    *    *    *    *    *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

          160       170       180       190       200
          *    *    *    *    *    *    *    *    *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

          210       220       230       240       250
          *    *    *    *    *    *    *    *    *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

          260       270       280       290       300
          *    *    *    *    *    *    *    *    *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

          310       320       330       340       350
          *    *    *    *    *    *    *    *    *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

          360       370       380       390       400
          *    *    *    *    *    *    *    *    *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

```
            410         420         430        440         450
          *    *      *    *      *    *     *    *      *    *
     GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
     CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
     ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>


            460         470         480        490         500
          *    *      *    *      *    *     *    *      *    *
     ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
     TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
     AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>


            510         520         530        540         550
          *    *      *    *      *    *     *    *      *    *
     CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
     GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
     LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>


            560         570         580        590         600
          *    *      *    *      *    *     *    *      *    *
     CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
     GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
     GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>


            610         620         630        640         650
          *    *      *    *      *    *     *    *      *    *
     CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
     GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
     SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>


            660         670         680        690         700
          *    *      *    *      *    *     *    *      *    *
     TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
     AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
     SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>


            710         720         730        740         750
          *    *      *    *      *    *     *    *      *    *
     CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
     GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
     PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>


            760         770         780        790         800
          *    *      *    *      *    *     *    *      *    *
     CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
     GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
     ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>


            810         820         830        840         850
          *    *      *    *      *    *     *    *      *    *
     AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
     TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
     SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
```

```
          860        870        880         890        900
     *     *     *     *    *     *     *  ·  *     *     *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
ArgAspLeu  ThrSerGlu  AspGlnIleVal LeuLeuLys SerSerAla>


          910        920        930         940        950
     *     *     *     *    *     *     *     *     *     *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>


          960        970        980         990        1000
     *     *     *     *    *     *     *     *     *     *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr  CysGlyAsnGln AspTyrLys TyrArgVal  SerAspValThr>


          1010       1020       1030        1040       1050
     *     *     *     *    *     *     *  ·  *     *     *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
LysAlaGly  HisSerLeu  GluLeuIleGlu ProLeuIle LysPheGln>


          1060       1070       1080        1090       1100
     *     *     *     *    *     *     *     *     *     *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>


          1110       1120       1130        1140       1150
     *     *     *     *    *     *  .  *     *     *     *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys  IleValSerPro AspArgPro GlyValGln  AspAlaAlaLeu>


          1160       1170       1180        1190       1200
     *     *     *     *    *     *     *     *     *     *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
IleGluAla  IleGlnAsp  ArgLeuSerAsn ThrLeuGln ThrTyrIle>


          1210       1220       1230        1240       1250
     ·*    *     *     *    *     *     *     *     *     *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>


          1260       1270       1280        1290       1300
     *     *     *     *    *     *     *     *     *     *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu  AlaAspLeuArg SerLeuAsn GluGluHis  SerLysGlnTyr>
```

```
          1310           1320            1330            1340            1350
      *         *      *         *      *         *      *         *      *         *
    CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
    GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
    ArgCysLeu  SerPheGln  ProGluCysSer MetLysLeu  ThrProLeu>

                1360           1370            1380
           *         *      *         *      *         *
         TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA
         ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT
         ValLeuGluVal PheGlyAsn  GluIleSer ***>
```

FIGURE 7   TRANSCRIPT 10

(Sequence Range: 1 to 1534)

```
               10          20          30          40          50
     *       *      *      *      *      *      *      *      *      *
     GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
     CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                      MetGluTrpArg AsnLysLys>

               60          70          80          90         100
     *       *      *      *      *      *      *      *      *      *
     AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
     TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
     ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

              110         120         130         140         150
     *       *      *      *      *      *      *      *      *      *
     GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
     CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
     GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

              160         170         180         190         200
     *       *      *      *      *      *      *      *      *      *
     GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
     CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
     ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

              210         220         230         240         250
     *       *      *      *      *      *      *      *      *      *
     CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
     GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
     HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***

              260         270         280         290         300
     *       *      *      *      *      *      *      *      *      *
     CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
     GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

              310         320         330         340         350
     *       *      *      *      *      *      *      *      *      *
     TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
     AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

              360         370         380         390         400
     *       *      *      *      *      *      *      *      *      *
     CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
     GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

```
          410        420        430        440        450
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

          460        470        480        490        500
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

          510        520        530        540        550
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

          560        570        580        590        600
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

          610        620        630        640        650
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

          660        670        680        690        700
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

          710        720        730        740        750
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

          760        770        780        790        800
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

          810        820        830        840        850
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

          860        870        880        890        900
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

          910        920        930        940        950
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
```

```
            960        970        980        990        1000
         *      *    *      *    *      *    *      *    *      *
       TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
       AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

           1010       1020       1030       1040       1050
         *      *    *      *    *      *    *      *    *      *
       TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
       AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

           1060       1070       1080       1090       1100
         *      *    *      *    *      *    *      *    *      *
       CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
       GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

           1110       1120       1130       1140       1150
         *      *    *      *    *      *    *      *    *      *
       TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
       ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

           1160       1170       1180       1190       1200
         *      *    *      *    *      *    *      *    *      *
       ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
       TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

           1210       1220       1230       1240       1250
         *      *    *      *    *      *    *      *    *      *
       GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
       CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

           1260       1270       1280       1290       1300
         *      *    *      *    *      *    *      *    *      *
       TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
       ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

           1310       1320       1330       1340       1350
         *      *    *      *    *      *    *      *    *      *
       CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
       GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

           1360       1370       1380       1390       1400
         *      *    *      *    *      *    *      *    *      *
       CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
       GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

           1410       1420       1430       1440       1450
         *      *    *      *    *      *    *      *    *      *
       TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
       AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

           1460       1470       1480       1490       1500
         *      *    *      *    *      *    *      *    *      *
       TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
       ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

```
              1510              1520              1530
           *       *        *       *        *       *
      TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA
      ACACGAGCTT CACAAACCGT TACTCTAGAG GACT
```

FIGURE 8   TRANSCRIPT 11

```
           10          20          30          40          50
            *           *           *           *           *
        TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
        ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC


           60          70          80          90         100
            *           *           *           *           *
        GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
        CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT


          110         120         130         140         150
            *           *           *           *           *
        AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
        TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG


          160         170         180         190         200
            *           *           *           *           *
        TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
        AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC


          210         220         230         240         250
            *           *           *           *           *
        CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
        GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG


          260         270         280         290         300
            *           *           *           *           *
        ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
        TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                                    MetGluAla>


          310         320         330         340         350
            *           *           *           *           *
        TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
        ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
        MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>


          360         370         380       , 390         400
            *           *           *           *           *
        CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
        GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
        ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>


          410         420         430         440         450
            *           *           *           *           *
        TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
        ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
         AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>


          460         470         480         490         500
            *           *           *           *           *
        GGAAGGCACT ATTCACCTGC CCCTTCAACG GGACTGCCG CATCACCAAG
        CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
        ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
```

```
          510        520        530        540        550
           *          *          *          *          *
       GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
       CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
       AspAsnArg  ArgHisCysGln AlaCysArg LeuLysArg  CysValAspIle>


          560        570        580        590        600
           *          *          *          *          *
       CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
       GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
        GlyMetMet  LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>


          610        620        630        640        650
           *          *          *          *          *
       GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
       CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
       ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>


          660        670        680        690        700
           *          *          *          *          *
       CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
       GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
       ArgProLys  LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>


          710        720        730        740        750
           *          *          *          *          *
       CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
       GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
        AlaHisHis LysThrTyr AspProThrTyr SerAspPhe  CysGlnPhe>


          760        770        780        790        800
           *          *          *          *          *
       GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
       CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
       ArgProProVal ArgValAsn AspGlyGly  GlySerHisPro SerArgPro>


          810        820        830        840        850
           *          *          *          *          *
       AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
       TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
       AsnSerArg  HisThrProSer PheSerGly AspSerSer  SerSerCysSer>


          860        870        880        890        900
           *          *          *          *          *
       AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
       TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
       AspHisCys  IleThrSer SerAspMetMet AspSerSer  SerPheSer>


          910        920        930        940        950
           *          *          *          *          *
       ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
       TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
       AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>


          960        970        980        990       1000
           *          *          *          *          *
       CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
       GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
       LeuSerGln  LeuSerMetLeu ProHisLeu AlaAspLeu  ValSerTyrSer>
```

```
                               1010          1020          1030          1040          1050
                                *             *             *             *             *
              CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
              GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
              IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

                               1060          1070          1080          1090          1100
                                *             *             *             *             *
              TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
              AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
              LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

                               1110          1120          1130          1140          1150
                                *             *             *             *             *
              ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
              TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
              IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

                               1160          1170          1180          1190          1200
                                *             *             *             *             *
              CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
              GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
              CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

                               1210          1220          1230          1240          1250
                                *             *             *             *             *
              GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
              CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
              GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

                               1260          1270          1280          1290          1300
                                *             *             *             *             *
              AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
              TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
              LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

                               1310          1320          1330          1340          1350
                                *             *             *             *             *
              CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
              GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
              IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

                               1360          1370          1380          1390          1400
                                *             *             *             *             *
              CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
              GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
              AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

                               1410          1420          1430          1440          1450
                                *             *             *             *             *
              CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
              GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
              HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

                               1460          1470          1480          1490          1500
                                *             *             *             *             *
              AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
              TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
              AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

```
        1510          1520          1530          1540          1550
          *             *             *             *             *
      TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
      AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
      LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>


        1560          1570
          *             *

      GTGTTTGGCA ATGAGATCTC CTGA
      CACAAACCGT TACTCTAGAG GACT
      ValPheGly AsnGluIleSer ***>
```